RAW SEQUENCE LISTING   DATE: 07/27/2004
PATENT APPLICATION: US/09/303,232C   TIME: 11:45:23

Input Set : A:\Mo5176new_rev.txt
Output Set: N:\CRF4\07272004\I303232C.raw

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 2 <110> APPLICANT: Bayer Aktiengesellschaft
 4 <120> TITLE OF INVENTION: Nucleic Acids which encode
 5        insect acetylcholine receptor subunits
 7 <130> FILE REFERENCE: Le A 33 020-Foreign Countries
 9 <140> CURRENT APPLICATION NUMBER: US/09/303,232C
10 <141> CURRENT FILING DATE: 1999-04-30
12 <150> PRIOR APPLICATION NUMBER: DE 198 19 829.9
13 <151> PRIOR FILING DATE: 1998-05-04
15 <160> NUMBER OF SEQ ID NOS: 14
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2886
21 <212> TYPE: DNA
22 <213> ORGANISM: Drosophila melanogaster
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (372)..(2681)
28 <400> SEQUENCE: 1
29 ggcacgagaa aaagttgtgg tataaacttt tattgtagga aaacgcataa aaataataga 60
31 aaaacgctct tcgggttgta aagaaaataa gaagacaaaa gaaagacatg aaaacgttgc 120
33 aaacaataaa gcatatactt gccatattga tataaaggga aatcgtgaaa aggcggtgaa 180
35 aatttcgtaa gattagttgg tattaagggc agcccatgca cacagctaaa aagggaacta 240
37 aaaaaacccc gcacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300
39 aattatatta ttgtaatcta gtagagagca gacaacatat ccgctggcaa caaccaacac 360
41 cgaaagagac t atg aaa aat gca caa ctg aaa ctg act gaa gtt gac gat  410
42              Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp
43                1                5                    10
45 gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt  458
46 Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe
47      15                   20                   25
49 agc agc agt agc agc aca aga acc acc agc agc aac cag agg cac aac  506
50 Ser Ser Ser Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn
51  30                   35                   40                   45
53 cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac  554
54 Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His
55                   50                   55                   60
57 agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca  602
58 Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala
59                   65                   70                   75
61 tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag  650
62 Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln
63          80                   85                   90
65 acg cat ctg caa cag cta gac agc agc aac atg ttg tcg cca aag aca  698
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RAW SEQUENCE LISTING   DATE: 07/27/2004
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Input Set : A:\Mo5176new_rev.txt
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66 Thr His Leu Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr
67      95                  100                  105
69 gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca    746
70 Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro
71 110                 115                  120                  125
73 aca aac ata aga ctg tgt gca cgc aag cga caa cga ttg cgt cgc cga    794
74 Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg
75                  130                  135                  140
77 cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa    842
78 Arg Lys Arg Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln
79              145                  150                  155
81 cag caa ctt agc atg cct ccc ttc aaa acg cgc aaa tcc acg gac acc    890
82 Gln Gln Leu Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr
83          160                  165                  170
85 tac agc aca cca gca gca aca acc agc tgt ccg aca gcc acc tac atg    938
86 Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met
87      175                  180                  185
89 caa tgt cga gcc agc gac aat gag ttc agt att ccg ata tcg aga cat    986
90 Gln Cys Arg Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His
91 190                 195                  200                  205
93 gat aga gta tcc acg gcc aca ttc gcc tgg gtg ttg cat gtg ctg cag   1034
94 Asp Arg Val Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln
95                  210                  215                  220
97 gtg ctg ctc gtg tcg ctg caa cag tgg caa ctt cac gtg caa cag cga   1082
98 Val Leu Leu Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg
99              225                  230                  235
101 tcg gtg cta ctg ttc aga agg atc gca gcg agc acc atc gcc ttc att   1130
102 Ser Val Leu Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile
103          240                  245                  250
105 tcc tat tta ggc agc ttt gca gcg caa ctg aaa aat agc agc agc agc   1178
106 Ser Tyr Leu Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser
107      255                  260                  265
109 agt agc agc agc aac agc agc aac aac agc agc acg caa ata tta aac   1226
110 Ser Ser Ser Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn
111 270                 275                  280                  285
113 gga ctt aat aaa cac tca tgg ata ttt tta ttg ata tat ttg aat tta   1274
114 Gly Leu Asn Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu
115                  290                  295                  300
117 tct gct aaa gtt tgc cta gca gga tat cat gaa aag aga ctg tta cac   1322
118 Ser Ala Lys Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His
119          305                  310                  315
121 gat ctt ttg gat cct tat aat aca cta gaa cgt ccc gtt ctc aat gaa   1370
122 Asp Leu Leu Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu
123          320                  325                  330
125 tcg gac ccg tta caa tta agc ttt ggt tta act tta atg caa att atc   1418
126 Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
127      335                  340                  345
129 gat gtg gac gag aaa aat caa ttg cta gtc act aat gtg tgg tta aaa   1466
130 Asp Val Asp Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys
```

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131 350                    355                   360                   365
133 ctg gag tgg aac gac atg aat ctc cgc tgg aac acc tcc gac tat ggc     1514
134 Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Tyr Gly
135                    370                   375                   380
137 gga gtt aag gat ctg cga ata ccg ccg cat cgc atc tgg aag ccg gac     1562
138 Gly Val Lys Asp Leu Arg Ile Pro Pro His Arg Ile Trp Lys Pro Asp
139                    385                   390                   395
141 gtg ctg atg tac aac agt gcg gat gag gga ttt gac ggc acc tac cag     1610
142 Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln
143            400                   405                   410
145 acg aac gtg gtg gtg cgg aac aac ggc tcg tgt cta tac gtt ccg ccg     1658
146 Thr Asn Val Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro
147    415                   420                   425
149 ggg atc ttc aag tcg acg tgc aag atc gac atc acg tgg ttc ccc ttc     1706
150 Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe
151 430                    435                   440                   445
153 gat gac cag cgg tgc gag atg aag ttc ggc agt tgg acc tac gac gga     1754
154 Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly
155                    450                   455                   460
157 ttc cag ctg gat tta caa tta caa gat gaa act ggc ggt gat atc agc     1802
158 Phe Gln Leu Asp Leu Gln Leu Gln Asp Glu Thr Gly Gly Asp Ile Ser
159                    465                   470                   475
161 agt tac gtg ctc aac ggc gag tgg gaa cta ctg ggt gtg ccc ggc aaa     1850
162 Ser Tyr Val Leu Asn Gly Glu Trp Glu Leu Leu Gly Val Pro Gly Lys
163            480                   485                   490
165 cgt aac gag atc tat tac aac tgc tgc ccg gaa ccc tat ata gac atc     1898
166 Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile
167    495                   500                   505
169 acc ttc gcc atc atc atc cgc cga cga aca ctg tac tat ttc ttc aac     1946
170 Thr Phe Ala Ile Ile Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn
171 510                    515                   520                   525
173 ctg atc ata cct tgt gta ctg att gcc tcc atg gcc ttg ctc gga ttc     1994
174 Leu Ile Ile Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe
175                    530                   535                   540
177 acc ctg ccg cca gat tcg ggt gaa aaa tta tcg ctg ggt gtt acc atc     2042
178 Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile
179                    545                   550                   555
181 ttg ctc tcg ctg acc gtg ttt ctg aat atg gtt gcc gag aca atg ccg     2090
182 Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro
183            560                   565                   570
185 gct act tcc gat gcg gtg cca ttg tgg ata cgc atc gtg ttt ttg tgc     2138
186 Ala Thr Ser Asp Ala Val Pro Leu Trp Ile Arg Ile Val Phe Leu Cys
187    575                   580                   585
189 tgg ctg cca tgg ata ttg cga atg agt cgc cca gga cga ccg ctg atc     2186
190 Trp Leu Pro Trp Ile Leu Arg Met Ser Arg Pro Gly Arg Pro Leu Ile
191 590                    595                   600                   605
193 cta gag ttc ccg acc acg ccc tgt tcg gac aca tcc tcc gag cgg aag     2234
194 Leu Glu Phe Pro Thr Thr Pro Cys Ser Asp Thr Ser Ser Glu Arg Lys
195                    610                   615                   620
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RAW SEQUENCE LISTING   DATE: 07/27/2004
PATENT APPLICATION: US/09/303,232C   TIME: 11:45:23

Input Set : A:\Mo5176new_rev.txt
Output Set: N:\CRF4\07272004\I303232C.raw

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197 cac cag ata ctc tcc gac gtt gag ctg aaa gag cgc tcg tcg aaa tcg   2282
198 His Gln Ile Leu Ser Asp Val Glu Leu Lys Glu Arg Ser Ser Lys Ser
199             625                 630                 635
201 ctg ctg gcc aac gta cta gac atc gat gat gac ttc cgg cac aat tgt   2330
202 Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Asn Cys
203             640                 645                 650
205 cgc ccc atg acg ccc ggc gga aca ctg cca cac aac ccg gct ttc tat   2378
206 Arg Pro Met Thr Pro Gly Gly Thr Leu Pro His Asn Pro Ala Phe Tyr
207     655                 660                 665
209 cgc acg gtt tat gga caa ggc gac gat ggc agc att ggg cca att ggc   2426
210 Arg Thr Val Tyr Gly Gln Gly Asp Asp Gly Ser Ile Gly Pro Ile Gly
211 670                 675                 680                 685
213 agc acc cga atg ccg gat gcg gtc acc cat cat acg tgc atc aaa tca   2474
214 Ser Thr Arg Met Pro Asp Ala Val Thr His His Thr Cys Ile Lys Ser
215             690                 695                 700
217 tca act gaa tat gaa tta ggt tta atc tta aag gaa att cgc ttt ata   2522
218 Ser Thr Glu Tyr Glu Leu Gly Leu Ile Leu Lys Glu Ile Arg Phe Ile
219             705                 710                 715
221 act gat cag cta cgt aaa gat gac gag tgc aat gac att gcc aat gat   2570
222 Thr Asp Gln Leu Arg Lys Asp Asp Glu Cys Asn Asp Ile Ala Asn Asp
223         720                 725                 730
225 tgg aaa ttt gca gct atg gtc gtt gac aga ctg tgc ctt atc ata ttc   2618
226 Trp Lys Phe Ala Ala Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe
227     735                 740                 745
229 aca atg ttc gca ata tta gcc aca ata gct gta cta cta tcg gca cca   2666
230 Thr Met Phe Ala Ile Leu Ala Thr Ile Ala Val Leu Leu Ser Ala Pro
231 750                 755                 760                 765
233 cat att att gtc tcg tagccatatg ggcgaggtgg ttattgttat tggttttatt   2721
234 His Ile Ile Val Ser
235                 770
237 ataaaatcaa tttgttaatt attaaattaa taacgaaact ctttaagtaa attaaaacta 2781
239 aaaagacact aaaaaagcac aaaaaaatag gaaaatacat gataaaaccc atgaactaaa 2841
241 taatacatcc aagaaaaacc aaaacaaaaa aaaaaaaaaa aaaaa                  2886
244 <210> SEQ ID NO: 2
245 <211> LENGTH: 770
246 <212> TYPE: PRT
247 <213> ORGANISM: Drosophila melanogaster
249 <400> SEQUENCE: 2
250 Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp Asp Glu Leu
251  1               5                  10                  15
253 Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe Ser Ser Ser
254             20                  25                  30
256 Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn Gln Gln Leu
257         35                  40                  45
259 Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His Ser Asn Ile
260     50                  55                  60
262 Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala Ser Lys Asp
263 65                  70                  75                  80
265 Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln Thr His Leu
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RAW SEQUENCE LISTING   DATE: 07/27/2004
PATENT APPLICATION: US/09/303,232C   TIME: 11:45:23

Input Set : A:\Mo5176new_rev.txt
Output Set: N:\CRF4\07272004\I303232C.raw

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266                    85             90                 95
268 Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr Ala Ala Ala
269              100            105              110
271 Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro Thr Asn Ile
272         115            120             125
274 Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg Arg Lys Arg
275     130            135              140
277 Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln Gln Gln Leu
278 145            150             155                160
280 Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr Tyr Ser Thr
281             165            170             175
283 Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met Gln Cys Arg
284         180            185             190
286 Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His Asp Arg Val
287         195            200            205
289 Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln Val Leu Leu
290     210            215            220
292 Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg Ser Val Leu
293 225            230            235                240
295 Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile Ser Tyr Leu
296             245            250             255
298 Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser Ser Ser Ser
299             260            265             270
301 Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn Gly Leu Asn
302         275            280            285
304 Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu Ser Ala Lys
305     290            295            300
307 Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His Asp Leu Leu
308 305            310            315                320
310 Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu Ser Asp Pro
311             325            330             335
313 Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile Asp Val Asp
314         340            345            350
316 Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys Leu Glu Trp
317     355            360            365
319 Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Tyr Gly Gly Val Lys
320     370            375            380
322 Asp Leu Arg Ile Pro Pro His Arg Ile Trp Lys Pro Asp Val Leu Met
323 385            390            395                400
325 Tyr Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln Thr Asn Val
326             405            410             415
328 Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe
329         420            425            430
331 Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe Asp Asp Gln
332         435            440            445
334 Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Phe Gln Leu
335     450            455            460
337 Asp Leu Gln Leu Gln Asp Glu Thr Gly Gly Asp Ile Ser Ser Tyr Val
338 465            470            475                480
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/27/2004
PATENT APPLICATION: US/09/303,232C   TIME: 11:45:24

Input Set : A:\Mo5176new_rev.txt
Output Set: N:\CRF4\07272004\I303232C.raw

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:7; N Pos. 6
Seq#:8; N Pos. 9

VERIFICATION SUMMARY   DATE: 07/27/2004
PATENT APPLICATION: **US/09/303,232C**   TIME: 11:45:24

Input Set : **A:\Mo5176new_rev.txt**
Output Set: **N:\CRF4\07272004\I303232C.raw**

L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0